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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/525,885DATE: 04/03/2000
TIME: 11:08:19

Input Set: I525885.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

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1 <110> APPLICANT: Hanson, Andrew D.
2 Nuccio, Michael L.
3 Henry, Susan A.
4 <120> TITLE OF INVENTION: POLYNUCLEOTIDE COMPOSITIONS ENCODING
5 S-ADENOSYL-L-METHIONINE: PHOSPHOETHANOLAMINE
6 N-METHYLTRANSFERASE AND METHODS FOR MODULATING LIPID
7 BIOSYNTHESIS IN PLANTS
8 <130> FILE REFERENCE: 4300.012700
9 <140> CURRENT APPLICATION NUMBER: US/09/525,885
10 <141> CURRENT FILING DATE: 2000-03-15
11 <160> NUMBER OF SEQ ID NOS: 8
12 <170> SOFTWARE: PatentIn Ver. 2.1
13 <210> SEQ ID NO 1
14 <211> LENGTH: 2235
15 <212> TYPE: DNA
16 <213> ORGANISM: Spinacia oleracea
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20 attgccatttggg agggtcaact atactttaa ctatctcctt cttttctttt cccacaattt 180
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29 tggatgttcaagatgttcatca atcaggagat cacaagcgca aaagcaatcc 720
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48 agttcatgga ctgtatatgc aaaatctacc aataagctgt gagttgcaaa ctgaaagatg 1860
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63 35 40 45
Leu Ser Met Leu Pro Pro Tyr Glu Gly Lys Ser Val Leu Glu Leu Gly
64 50 55 60
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66 85 90 95
Ile Asn Gly His Tyr Lys Asn Val Lys Phe Met Cys Ala Asp Val Thr
67 100 105 110
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69 130 135 140
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70 145 150 155 160
Glu Ser Cys Phe His Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro
71 165 170 175
Thr His Tyr Arg Glu Pro Arg Phe Tyr Thr Lys Ile Phe Lys Glu Cys
72 180 185 190
His Met Gln Asp Asp Ser Gly Asn Ser Tyr Glu Leu Ser Leu Ile Gly
73 195 200 205
Cys Lys Cys Ile Gly Ala Tyr Val Lys Ser Lys Lys Asn Gln Asn Gln
74 210 215 220
Ile Ser Trp Leu Trp Gln Lys Val Asp Ser Glu Asp Asp Lys Gly Phe
75 225 230 235 240
Gln Arg Phe Leu Asp Ser Ser Gln Tyr Lys Phe Asn Ser Ile Leu Arg
76 245 250 255
Tyr Glu Arg Val Phe Gly Pro Gly Tyr Val Ser Thr Gly Gly Leu Glu
77 260 265 270

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98          290           295           300
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100         305           310           315           320
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102          325           330           335
103      Phe Glu Val Ala Asp Cys Thr Lys Lys Asp Tyr Pro Glu Asn Ser Phe
104          340           345           350
105      Asp Val Ile Tyr Ser Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro
106          355           360           365
107      Ala Leu Phe Arg Ser Phe His Lys Trp Leu Lys Pro Gly Gly Lys Val
108          370           375           380
109      Leu Ile Ser Asp Tyr Cys Lys Ser Ala Gly Thr Pro Ser Ala Glu Phe
110          385           390           395           400
111      Ala Ala Tyr Ile Arg Gln Arg Gly Tyr Asp Leu His Asp Val Lys Ala
112          405           410           415
113      Tyr Gly Lys Met Leu Lys Asp Ala Gly Phe Val Glu Val Ile Ala Glu
114          420           425           430
115      Asn Arg Thr Asp Gln Phe Ile Gln Val Leu Gln Lys Glu Leu Asp Ala
116          435           440           445
117      Leu Glu Gln Glu Lys Asp Asp Phe Ile Asp Asp Phe Ser Glu Glu Asp
118          450           455           460
119      Tyr Asn Asp Ile Val Asp Gly Trp Lys Ala Lys Leu Val Arg Thr Thr
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130 attgccattt agggtcacta atacttttaa ctatctccctt cttttctttt cccacaattt 180
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141 aacccactac cgtgaaccta gggttctacac caagatcttc aaagaatgcc atatgcaaga 840
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143 caaaagcaag aagaatcaga accagataag ctgggttatgg cagaagttt gagctttagga 960
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156 Leu Asp Ser Gln Ala Ser Asp Leu Asp Lys Val Glu Arg Pro Glu Val
157 35 40 45
158 Leu Ser Met Leu Pro Pro Tyr Glu Gly Lys Ser Val Leu Glu Leu Gly
159 50 55 60
160 Ala Gly Ile Gly Arg Phe Thr Gly Glu Leu Ala Glu Lys Ala Ser Gln
161 65 70 75 80
162 Val Ile Ala Leu Asp Phe Ile Glu Ser Val Ile Lys Lys Asn Glu Ser
163 85 90 95
164 Ile Asn Gly His Tyr Lys Asn Val Lys Phe Met Cys Ala Asp Val Thr
165 100 105 110
166 Ser Pro Ser Leu Asn Ile Ser Pro Asn Ser Val Asp Ile Ile Phe Ser
167 115 120 125
168 Asn Trp Leu Leu Met Tyr Leu Ser Asp Glu Glu Val Glu Arg Leu Val
169 130 135 140
170 Glu Arg Met Leu Lys Trp Leu Lys Pro Gly Gly Tyr Ile Phe Phe Arg
171 145 150 155 160
172 Glu Ser Cys Phe His Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro
173 165 170 175
174 Thr His Tyr Arg Glu Pro Arg Phe Tyr Thr Lys Ile Phe Lys Glu Cys
175 180 185 190
176 His Met Gln Asp Asp Ser Gly Asn Ser Tyr Glu Leu Ser Leu Ile Gly
177 195 200 205
178 Cys Lys Cys Ile Gly Ala Tyr Val Lys Ser Lys Lys Asn Gln Asn Gln
179 210 215 220
180 Ile Ser Trp Leu Trp Gln Lys Val Asp Ser Glu Asp Asp Lys Gly Phe
181 225 230 235 240
182 Gln Arg Phe Leu Asp Ser Ser Gln Tyr Lys Phe Asn Ser Ile Leu Arg
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214 <400> SEQUENCE: 7 9
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**VERIFICATION SUMMARY
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Line ? Error/Warning

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